```
OM of: US-09-525-998A-11 to: SwissProt_39:*   out_format : pfs

Date: Apr 23, 2002 10:31 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
  -MODEL=frame+_n2p.model -DEV-xlp
  -Q=/cgn2_1/USPTO_spool/US09525998/runat_23042002_132339_10295/app_query fasta_1 2117
  -DB-SwissProt_39 -QFMT-fastan -SUFFIX-rsp -GAPOP-12.000
  -GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT=0.000
  -QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT=0.500
  -FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
  -DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
  -TRANS-human40.cdi -LIST-45 -DOCALIGN 200  THR_SCORE pct
  -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT=pfs
  -NORM-ext -MINLEN-0 -MAXLEN-2000000000
  -USER-US09525998_@CGN1_1_43 -NCPU-6 -ICPU=3 -LONGLOG -NO_XLPXY
  -WAIT -THREADS-1

Search information block:
Query: US-09-525-998A-11
Query length: 600
Database: SwissProt_39:*
Database sequences: 100059
Database length: 36664827
Search time (sec): 87.870000



score_list:
Sequence                 Strd Orig     ZScore    EScore Len  ! Documentation  ..
SwissProt_39:TNR1_HUMAN + 1117.50 1764.17  3.0e-91    455  ! P19438 homo sapiens (human).
SwissProt_39:TNR1_PIG +    822.00 1294.73  4.1e-65    461  ! P50555 sus scrofa (pig)  tumor
SwissProt_39:TNR1_MOUSE +  787.00 1239.27  5.2e-62    454  ! P25118 mus musculus (mouse).
SwissProt_39:TNR1_RAT +    774.50 1219.29  6.6e-61    461  ! P22934 rattus norvegicus (rat)
SwissProt_39:TNR1_BOVIN +  772.00 1215.13  1.1e-60    471  ! O19131 bos taurus (bovine).
SwissProt_39:TNRC_HUMAN +  213.50  328.79  2.8e-11    435  ! P36941 homo sapiens (human).
SwissProt_39:WSL1_HUMAN +  209.50  322.80  6.3e-11    417  ! Q93038 h wsl 1 protein prec
SwissProt_39:NGFR_HUMAN +  207.50  319.42  9.5e-11    427  ! P08138 homo sapiens (human).
SwissProt_39:NGFR_RAT +    193.50  297.22  1.6e-09    425  ! P07174 rattus norvegicus (rat)
SwissProt_39:VT2_SFVKA +   190.50  294.78  2.9e-09    325  ! P25943 shope fibroma virus (s
SwissProt_39:VT2_MYXVL +   187.50  289.99  5.4e-09    326  ! P29825 myxoma virus (strain l
SwissProt_39:TNR2_MOUSE +  181.00  276.43  2.1e-08    474  ! P25119 mus musculus (mouse).
SwissProt_39:TNRC_MOUSE +  180.00  275.99  2.6e-08    415  ! P50284 mus musculus (mouse).
SwissProt_39:FASA_PIG +    176.50  272.36  5.1e-08    332  ! O77736 sus scrofa (pig). fasl
SwissProt_39:CD40_BOVIN +  173.00  268.62  1.0e-07    269  ! Q28203 bos taurus (bovine).
SwissProt_39:CD40_MOUSE +  170.50  264.93  1.7e-07    289  ! P27512 mus musculus (mouse).
SwissProt_39:FASA_MOUSE +  169.50  261.37  2.1e-07    327  ! P25446 mus musculus (mouse).
SwissProt_39:FASA_BOVIN +  166.50  256.71  3.9e-07    323  ! P51867 bos taurus (bovine).
SwissProt_39:VC22_VARV +   164.00  252.07  6.5e-07    349  ! P34015 variola virus  protein
SwissProt_39:TNR2_HUMAN +  162.50  247.29  9.1e-07    461  ! P20333 homo sapiens (human).
SwissProt_39:CD27_MOUSE +  154.50  239.87  4.4e-06    250  ! P41272 mus musculus (mouse).
SwissProt_39:CD27_HUMAN +  119.00  232.79  1.3e-05    260  ! P26842 homo sapiens (human).
SwissProt_39:FASA_RAT +    149.00  228.89  1.4e-05    324  ! Q63199 rattus norvegicus (rat)
SwissProt_39:NGFR_CHICK +  148.00  225.14  1.7e-05    416  ! P18519 gallus gallus (chick
SwissProt_39:CD40_HUMAN +  146.00  225.48  2.5e-05    277  ! P25942 homo sapiens (human).
SwissProt_39:VS41_GIALA +  144.50  215.25  3.7e-05    687  ! P92127 giardia lamblia (giar
SwissProt_39:FUR2_DROME +  143.50  205.94  5.0e-05   1680  ! P30432 drosophila melanogas
SwissProt_39:TR14_HUMAN +  142.50  213.74  5.1e-05    283  ! Q92956 homo sapiens (human).
SwissProt_39:OX40_MOUSE +  137.50  212.14  0.0001     272  ! P47741 mus musculus (mouse).
SwissProt_39:PCK5_BRACL +  134.00  190.77  0.0003    1696  ! Q9nj15 branchiostoma calif
SwissProt_39:PCK5_MOUSE +  134.00  189.89  0.0004    1877  ! Q04592 mus musculus (mouse)
SwissProt_39:PCK5_HUMAN +  133.00  194.53  0.0004     913  ! Q92824 homo sapiens (human)
SwissProt_39:OX40_RAT +    131.50  202.64  0.0005     271  ! P15725 rattus norvegicus (rat)
SwissProt_39:CD30_HUMAN +  131.00  195.05  0.0006     595  ! P28908 homo sapiens (human).
SwissProt_39:FASA_HUMAN +  130.50  199.22  0.0006     335  ! P25445 homo sapiens (human).
SwissProt_39:LML2_CAEEL +  127.00  172.98  0.0016    3672  ! Q21313 caenorhabditis elega
SwissProt_39:OX40_HUMAN +  124.50  191.43  0.0020     277  ! P43489 homo sapiens (human).
SwissProt_39:NID3_MOUSE +  120.50  166.63  0.0056    2418  ! Q61982 mus musculus (mouse)
SwissProt_39:SL13_MOUSE +  119.00  182.54  0.0061     279  ! O70433 mus musculus (mouse).
SwissProt_39:OS24_PLABA +  117.50  182.49  0.0089     213  ! Q04620 plasmodium berghei (s
SwissProt_39:ISA4_GIALA +  117.50  172.05  0.0092     713  ! P21849 giardia lamblia (g
SwissProt_39:PAC4_HUMAN +  117.50  169.49  0.0095     969  ! P29122 homo sapiens (huma
SwissProt_39:TGFB_RAT +    117.00  163.69  0.0111    1712  ! Q00918 rattus norvegicus (
SwissProt_39:LDL2_XENLA +  116.50  168.52  0.0115     852  ! Q95088 xenopus laevis (af
SwissProt_39:SL13_RAT +    115.00  177.77  0.0112     279  ! O70115 rattus norvegicus (r

seq_name: SwissProt_39:TNR1_HUMAN

seq_documentation_block:
ID   TNR1_HUMAN     STANDARD;      PRT;   455 AA.
AC   P19438;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE   BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (TNF-RI) (P55) (CD120A).
GN   TNFRSF1A OR TNFR1 OR TNFAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=90235285; PubMed=2158863;
RA   Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA   Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;
RT   "Molecular cloning and expression of a receptor for human tumor
RT   necrosis factor.";
RL   Cell 61:361-370(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90235284; PubMed=2158862;
RA   Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
RA   Tabuchi H., Lesslauer W.;
RT   "Molecular cloning and expression of the human 55 kd tumor necrosis
RT   factor receptor.";
RL   Cell 61:351-359(1990).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 41-57, 110-124 AND 199-201.
RX   MEDLINE=91066021; PubMed=1698610;
RA   Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,
RA   Aderka D., Holtmann H., Wallach D.;
RT   "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT   for the type I TNF-R, cloned using amino acid sequence data of its
RT   soluble form, encodes both the cell surface and a soluble form of the
RT   receptor.";
RL   EMBO J. 9:3269-3278(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91090841; PubMed=1702293;
RA   Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA   Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=91022853; PubMed=2170474;
RA   Gray P.W., Barrett K., Chantry D., Turner M., Feldmann M.;
RT   "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
RT   expression of recombinant soluble TNF-binding protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92250945; PubMed=1315717;
RA   Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;
RT   "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RT   localization to chromosome 12p13.";
RL   Genomics 13:219-224(1992).
RN   [7]
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RP   SEQUENCE OF 41-45.
RX   MEDLINE-90110215; PubMed-2153136;
RA   Engelmann H., Novick D., Wallach D.;
RT   "Two tumor necrosis factor-binding proteins purified from human
RT   urine. Evidence for immunological cross reactivity with cell surface
RT   tumor necrosis factor receptors.";
RL   J. Biol. Chem. 265:1531-1536(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.
RX   MEDLINE=93258809; PubMed=8387891;
RA   Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H. J.,
RA   Broger C., Loetscher H., Lesslauer W.;
RT   "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT   beta complex: implications for TNF receptor activation.";
RL   Cell 73:431-445(1993).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE=97094982; PubMed=8939750;
RA   Naismith J.H., Devine T.Q., Kohno H., Sprang S.R.;
RT   "Structures of the extracellular domain of the type I tumor necrosis
RT   factor receptor.";
RL   Structure 4:1251-1262(1996).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF
CC       NONCYTOCIDAL TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION
CC       OF THE ACID SPHINGOMYELINASE.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
CC       THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
CC       NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X55313; CAA39021.1; -.
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DR   EMBL; M58286; AAA36753.1; -.
DR   EMBL; M63121; AAA36754.1; -.
DR   EMBL; M75866; AAA61201.1; -.
DR   EMBL; M75864; AAA61201.1; JOINED.
DR   EMBL; M75865; AAA61201.1; JOINED.
DR   EMBL; M60275; AAA36756.1; -.
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DR   PIR; A34899; GQHUT1.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1NCF; 07-DEC-95.
DR   PDB; 1EXT; 11-JAN-97.
DR   MIM; 191190; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;
KW   3D-structure.
FT   SIGNAL       1    21
FT   CHAIN       22   455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   CHAIN       41   291       TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN      22   211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212   234       POTENTIAL.
FT   DOMAIN     235   455       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      43   196       4 X TNFR-CYS.
FT   REPEAT      43    82       TNFR-CYS 1.
FT   REPEAT      83   125       TNFR-CYS 2.
FT   REPEAT     126   166       TNFR-CYS 3.
FT   REPEAT     167   196       TNFR-CYS 4.
FT   DOMAIN     338   348       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     356   441       DEATH.
FT   DISULFID    44    58
FT   DISULFID    59    72
FT   DISULFID    62    81
FT   DISULFID    84    99
FT   DISULFID   102   117
FT   DISULFID   105   125
FT   DISULFID   127   143
FT   DISULFID   146   158
FT   DISULFID   149   166
FT   DISULFID   168   179
FT   DISULFID   182   191
FT   DISULFID   185   195
FT   CARBOHYD    54    54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   145   145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   151   151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   412   412       MISSING (IN REF. 4).
FT   CONFLICT   443   446       GPAA -> APP (IN REF. 4).
SQ   SEQUENCE   455 AA;  50494 MW;  4CEFBA96D03B8225 CRC64;


alignment_scores:
            Quality: 1117.50              Length:    211
              Ratio:  5.588                Gaps:        1
 Percent Similarity:  94.787   Percent Identity: 94.787

alignment_block:
 US-09-525-998A-11 x TNR1_HUMAN   ..

 Align seg 1/1  to: TNR1_HUMAN  from: 1  to: 455

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       1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17

      51 GCTGTTCGTGGGAATATACCCCTCAGGGGTTATTGGA..............  87
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      17 aLeuLeuValGlyIleTyrProSerGlyValIleGlyLeuValProHisL 34

      88          .........GATAGTGTGTGTCCCAAGGAAAATATATC 117
                           |||||||||||||||||||||||||||||
      34 euGlyAspArgGluLysArgAspSerValCysProGlnGlyLysTyrIle 50

     118 CACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 167
         |||||||||||||||||||||||||||||||||||||||||||||||||
      51 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 67

     168 CTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGACT 217
         |||||||||||||||||||||||||||||||||||||||||||||||||
      67 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC 84
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218 GTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCACACACTGCCTC 267
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 84 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100

268 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 317
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 117

318 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGC 367
    ||||||||||||||||||||||||||||||||||||||||||||||||||
117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134

368 ATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 417
    ||||||||||||||||||||||||||||||||||||||||||||||||||
134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150

418 AATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCAC 467
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 167

468 CTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTA 517
    ||||||||||||||||||||||||||||||||||||||||||||||||||
167 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 184

518 ACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 567
    ||||||||||||||||||||||||||||||||||||||||||||||||||
184 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200

568 AATGTTAAGGGCACTGAGGACTCAGGCACCACA 600
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201 AsnValLysGlyThrGluAspSerGlyThrThr 211
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seq_name: SwissProt_39:TNR1_PIG

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seq_documentation_block:
ID   TNR1_PIG       STANDARD;      PRT;   461 AA.
AC   P50555;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-RI)
DE   (P55).
GN   TNFRSF1A OR TNFR1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=96011645; PubMed=7590278;
RA   Suter B., Pauli U.H.;
RT   "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
RT   receptor.";
RL   Gene 163:263-266(1995).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; U19994; AAC48499.1; -.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211    233       POTENTIAL.
FT   DOMAIN      234    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    195       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    195       TNFR-CYS 4.
FT   DOMAIN      340    350       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      362    447       DEATH.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    190       BY SIMILARITY.
FT   DISULFID    185    194       BY SIMILARITY.
FT   CARBOHYD     54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    145    145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   461 AA;  50696 MW;  CD72361EC6089D43 CRC64;

alignment_scores:
          Quality:  822.00         Length:    211
            Ratio:  4.676            Gaps:      2
 Percent Similarity:  83.412   Percent Identity:  69.668

alignment_block:
 US 09 525 998A 11 x TNR1_PIG ..

 Align seg 1/1  to: TNR1_PIG  from: 1  to: 461

      1 ATGGGGCTCTCTACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGA 50
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      1 MetGlyLeuSerThrValProGlyLeuLeuLeuProLeuValLeuArgAl 17

     51 GCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGA............ 87
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     17 aLeuLeuValAspValTyrProAlaGlyValHisGlyLeuValLeuHisP 34

     88 ....................GATAGTGTGTGTCCCCAAGGAAAATATATC 117
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      84 roGlyAspArgG'uLysArgGluSerLeuCysProGlnGlyLysTyrSer 50

     118 CACCCTCAAAATAATTCGATTGCTGTACCAAGTGCCACAAAGGAACCTA 167
         ||||||||||||:::|||||||||||||||||||||||||||||||||||
      51 HisProGlnAsnArgSerIleCysCysThrLysCysHisLysGlyThrTy 67

     168 CTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGACTCCAGCGACT 217
         |||||:::||||||||   |||||||||   ||||||||||||||||||
      67 rLeuHisAsnAspCysLeuGlyProGlyLeuAspThrAspCysArgGluC 84

     218 GTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 267
         ||:::::|||:::|||||||||||||||||||||||   :::||||||
      84 ysAspAsnGlyThrPheThrAlaSerGluAsnHisLeuThrGlnCysLeu 100

     268 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 317
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     101 SerCysSerLysCysArgSerGluMetSerGlnValGlulleSerProCy 117

     318 CACAGTGCACCGCGACACCGTGTGTGCCTCCAGCAAGAACCACTACCGCC 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgL 134

     368 ATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 417
           ||||||||||||:::|||||||||||||:::|||||||||||||||
     134 ysTyrTrpSerGluThrLeuPheGlnCysLeuAsnCysSerLeuCysPro 150

     418 AATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCAC 467
         ||||||||||||:::|||   |||   ||||||||||:::|||:::|||
     151 AsnGlyThrValGlnLeuProCysLeuGluLysGlnAspThrIleCysAs 167

     468 CTGCCATGCAGGTTTCTTTCTAACAGCAAAACCAGTGTGTCTCCTGTAGTA 517
         :|||||||:::|||||||||||||||||:::::|||||||||||||||   |
     167 nCysHisSerGlyPhePheLeuArgAspLysGluCysValSerCysValA 184

     518 ACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCCACCCCAGATTGAG 567
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     184 snCysLysAsnAla...AspCysLysAsnLeuCysProAlaThrSerGlu 199

     568 AATGTTAAGGGCACTGAGGACTCAGGCACCACA 600
         :::   :::      ::::|||:::||||||||
     200 ThrArgAsnAspPheGlnAspThrGlyThrThr 210

seq_name: SwissProt_39:TNR1_MOUSE

seq_documentation_block:
ID   TNR1_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   20 AUG-2001 (Rel. 40, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-RI)
DE   (P55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246168; PubMed=1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91285014; PubMed=1647956;
RA   Barrett K., Taylor Fishwick D.A., Cope A.P., Kissonerghis A.M.,
RA   Gray P.W., Feldmann M., Foxwell B.M.J.;
RT   "Cloning, expression and cross-linking analysis of the murine p55
RT   tumor necrosis factor receptor.";
RL   Eur. J. Immunol. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=92039815; PubMed=1657766;
RA   Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
RT   "Molecular cloning and expression of the mouse Tnf receptor type b.";
RL   Immunogenetics 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94245292; PubMed=8188324;
RA   Rebo B.F., Linthicum D.S.;
RT   "Nucleotide sequence of the TNF type I receptor from a mouse
RT   endothelioma cell line.";
RL   Immunogenetics 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93156721; PubMed=8381516;
RA   Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;
RT   "Genomic organization and promoter function of the murine tumor
RT   necrosis factor receptor beta gene.";
RL   Mol. Immunol. 30:165-175(1993).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60468; AAA39751.1; -.
DR   EMBL; M59377; AAA40464.1; -.
DR   EMBL; X59238; CAA41922.1; -.
DR   EMBL; X57796; CAA40936.1; -.
DR   EMBL; L26349; AAA59361.1; -.
DR   EMBL; M76656; AAA40465.1; -.
DR   EMBL; M88067; AAA40465.1; JOINED.
DR   EMBL; M76655; AAA40465.1; JOINED.
DR   PIR; A38634; GQMST1.
DR   PIR; S16677; S16677.
DR   PIR; S19021; S19021.
DR   HSSP; P19438; 1EXT.
DR   MGD; MGI:1314884; Tnfrsf1a.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
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DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    454       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN      22    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213   235       POTENTIAL.
FT   DOMAIN      236   454       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43   196       4 X TNFR-CYS.
FT   REPEAT       43    82       TNFR-CYS 1.
FT   REPEAT       83   125       TNFR-CYS 2.
FT   REPEAT      126   166       TNFR-CYS 3.
FT   REPEAT      167   196       TNFR-CYS 4.
FT   DOMAIN      339   349       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      356   441       DEATH.
FT   DISULFID     44    58       BY SIMILARITY.
FT   DISULFID     59    72       BY SIMILARITY.
FT   DISULFID     62    81       BY SIMILARITY.
FT   DISULFID     84    99       BY SIMILARITY.
FT   DISULFID    102   117       BY SIMILARITY.
FT   DISULFID    105   125       BY SIMILARITY.
FT   DISULFID    127   143       BY SIMILARITY.
FT   DISULFID    146   158       BY SIMILARITY.
FT   DISULFID    149   166       BY SIMILARITY.
FT   DISULFID    168   179       BY SIMILARITY.
FT   DISULFID    182   191       BY SIMILARITY.
FT   DISULFID    185   195       BY SIMILARITY.
FT   CARBOHYD     54    54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151   151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    252   252       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    394   394       R -> G (IN REF. 6).
SQ   SEQUENCE   454 AA;  50128 MW;  0719C2B8C3C2B6D9 CRC64;


alignment_scores:
            Quality:  787.00              Length:    211
              Ratio:  4.523                 Gaps:      2
 Percent Similarity:  82.464   Percent Identity: 66.351

alignment_block:
 US-09-525-998A-11 x TNR1_MOUSE  ..

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      34 euGlyAspArgGluLysArgAspSerLeuCysProGlnGlyLysTyrVal 50

     118 CACCCTCAAAATAATTCGATTIGCTGTACCAAGTGCCACAAAGGAACCTA 167
         |||   :::|||||||||||||||||||||||||||||||||||||||||
      51 HisSerLysAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 67

     168 CTTGTACAATGACTGTCCAGGCCGGGGCAGGAIACGGACTGCAGGAGI 217
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      67 rLeuValSerAspCysProSerProGlyArgAspThrValCysArgGluC 81

     218 GTGAGAGCGGCTCCTICACCGATTCAGAAAACCACCTCAGACACTGCCTC 267
         ||||||:::|||:::|||||||||||||||:::|||::|||||||:::|||||
      84 ysGluLysGlyThrPheThrAlaSerGlnAsnTyrLeuArgGlnCysLeu 100

     268 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 317
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         |||||||:::   |||||||||||||||:::|||||||||||||||   ||
     101 SerCysLysThrCysArgLysGluMetSerGlnValGluIleSerProCy 117

     318 CACAGIGGACGGGACACCGIGIGIGCCIGCAGAAGAACAGIACCGGC 467
         |   :::|||:::|||||||||||||||.:::::|||||||||||||
     117 sGlnAlaAspLysAspThrValCysGlyCysLysGluAsnGlnPheGlnA 134

     368 AIIAIIGGAGIGAAAACCTTTICCAGIGCTICAAIIGCAGCCICIGCCIC 417
         ::|||   |||| |:::   |||||||||   :::|||||   |:::::
     134 rgTyrLeuSerGluThrHisPheSerCysValAspCysSerIleCysPhe 150

     418 AATGGGACCGIGCACCICTCCIGCCAGGACAAACAGAACACCGIGIGCAC 467
         ||||||||||.||   :::   |||:::|||   |||||||||||||||:::
     151 AsnGlyThrVal hrIleProCysLysGluThrGlnAsnThrValCysAs 167

     468 CIGCAIGCAGG.IICIIICIAAGAGAAAAC.AGIGIGIGIC.IGTAGIA 517
         :|||||||||| ||||:|||||||||.:::|||||||:   ||||::
     167 nCysHisAlaGlyPhePheLeuArgGluSerGlnCysValProCysSerH 184

     518 ACICIAAGAAAAGCCIGGACIGCACGAACIIGIGCCIA...CCCCAGAII 564
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     184 isCysLysLysAsnGluGluCysMetLysLeuCysLeuProProProLeu 200

     565 GAGAAIGIIAAGGGCACICAGGACICAGGCACC 597
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     201 AlaAsnValThrAsnProGlnAspSerGlyThr 211

seq_name: SwissProt_49:TNR1_RAT

seq_documentation_block:
ID   TNR1_RAT       STANDARD;      PRT;   461 AA.
AC   P22984;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-MAR 1996 (Rel. 31, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-RI)
DE   (P55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 91090841; PubMed 1702293;
RA   Himmler A., Maurer-Fogy I., Kroenke M., Scherrich P., Pfizenmaier K.,
RA   Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE TRADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NEW MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAF2, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A CA NGFR/TNFR TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------- -- ----- ---------- ---- ----------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M63122; AAA42256.1; -.
DR   PIR; B36555; B36555.
DR   HSSP; P19438; 1TNF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor, Transmembrane, Glycoprotein, Repeat, Signal, Apoptosis.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    234       POTENTIAL.
FT   DOMAIN      235    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       84    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      344    354       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      363    448       DEATH.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    191       BY SIMILARITY.
FT   DISULFID    185    195       BY SIMILARITY.
FT   CARBOHYD     54     54       N-LINKED (GLCNAC      ) (POTENTIAL)
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   461 AA;  50969 MW;  EB23C05450FB1202 CRC64;


alignment_scores:
            Quality:  774.50              Length:    210
              Ratio:  4.583                 Gaps:      1
 Percent Similarity:  80.476   Percent Identity: 64.762

alignment_block:
 US-09-525-998A-11 x TNR1_RAT   ..

 Align seq 1/1  to: TNR1_RAT  from: 1  to: 461

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      51 GCTGTTGCTTCCCAATATACCCCTCAGGGCTTATTGGA..............  87
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      17 aLeuLeuMetGlyIleHisProSerGlyValThrGlyLeuValProSerL  34

      88 ....................GATAGTGTGTGTCCCCAAGGAAAATATATC 117
                             |||.....|||||||||||||||||||
      34 euGlyAspArgGluLysArgAspAsnLeuCysProCysGlyGlyTyrAla  50

     118 CACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 167
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      51 HisProLysAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy  67

     168 CTTGTACAATGACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGT 217
         ||||   :::|||||||||:::|||||||||:::|||   |||:::   |
      67 rLeuValSerAspCysProSerProGlyGlnGluThrValCysGluValC  84

     218 GTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 267
         ||.....|||...|||||||||||...|||||:::|||:::||||||
      84 ysAspLysGlyThrPheThrAlaSerGlnAsnHisValArgGlnCysLeu 100

     268 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 317
         ||||||:::   ||||||||||||||   ||||||||||||||   ||
     101 SerCysLysThrCysArgLysGluMetPheGlnValGluIleSerProCy 117

     318 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGC 367
         |   :::|||   |||||||||||||||||:::|||||||||:::::::
     117 sLysAlaAspMetAspThrValCysGlyCysLysLysAsnGlnPheGlnA 134

     368 AITATTGGAGTGAAAACCTTTGCCAGTGCTTCAATTGCAGCCTCTGCCTC 417
         ::|||   ||||||:::   |||||||||   :::||||||   |||:::
     134 rqTyrLeuSerGluThrHisPheGlnCysValAspCysSerProCysPhe 150

     418 AATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCAC 467
         ||||||||||||   :::   |||...|||||||||||||||||||||::
     151 AsnGlyThrValThrIleProCysLysGluLysGlnAsnThrValCysAs 167

     468 CTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTA 517
         :|||||||||||||||||||||      ||||||||:::   ||||||:
     167 nCysHisAlaGlyPhePheLeuSerGlyAsnGluCysThrProCysSerH 184

     518 ACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 567
         ::||||||||...   ||||||   |||||||||||||||   :::
     184 isCysLysLysAsnGlnGluCysMetLysLeuCysLeuProProValAla 200

     568 AATGTTAAGGGCACTGAGGACTCAGGCACC 597
         ||||||   :::   :::|||||||||||||
     201 AsnValThrAsnProGlnAspSerGlyThr 210

seq_name: SwissProt_39:TNR1_BOVIN

seq_documentation_block:
ID   TNR1_BOVIN     STANDARD;      PRT;   471 AA.
AC   O19131;
DT   20-AUG-2001 (Rel. 40, Created)
DT   20-AUG-2001 (Rel. 40, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (T80) (TNF R1) (TNF RI)
DE   (P55).
GN   TNFRSF1A OR TNFR1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia, Pecora, Bovoidea;
OC   Bovidae, Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RA   Lee E.-K., Taylor M.J., Kehrli M.E.;
RT   "Cloning of cDNA encoding bovine tumor necrosis factor receptor I
RT   (TNF-RI).";
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION  ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
```

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CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U90937; AAB65143.1; -.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor, Transmembrane, Glycoprotein, Repeat, Signal, Apoptosis.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    471       TUMOR NECROSIS FACTOR RECEPTOR 1
FT   DOMAIN       22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211    233       POTENTIAL.
FT   DOMAIN      234    471       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    195       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    195       TNFR-CYS 4.
FT   DOMAIN      340    360       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      372    457       DEATH.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    190       BY SIMILARITY.
FT   DISULFID    185    194       BY SIMILARITY.
FT   CARBOHYD     54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    145    145       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC     ) (POTENTIAL).
SQ   SEQUENCE   471 AA;  51367 MW;  5243EF514DFE81C4 CRC64;


alignment_scores:
            Quality:  772.00              Length:    211
              Ratio:  4.568                 Gaps:      2
 Percent Similarity:  80.095   Percent Identity: 64.455

alignment_block:
 US-09-525-998A-11 x TNR1_BOVIN  ..

 Align seq 1/1  to: TNR1_BOVIN  from: 1  to: 471

       1 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGA 50
         |||||||||   |||||||||   ||||||||||||||||||||
       1 MetGlyLeuProThrValProGlyLeuLeuLeuProLeuValLeuProAl 17

      51 GCTGTTGGTGGGAATATACCCCTCAGGGTTATTGGA               87
         |||||||::   :::|||||::::||||||   |||
      17 alLeuLeuAlaAspValTyrProAlaGlyValGlnGlyLeuValProHisP 34

      88 ....................GATAGTGTGTGTCCCCAAGGAAAATATATAC 117
                             :::|||   |||||||:|:|::'|||
      34 roGlyAspLeuGluLysArgGluSerProCysProGlnGlyLysTyrAsn 50

     118 CACCCTCAAAATAATTCGATTTGTGTACCAAGTGCCACAAAGGAACCTA 167
         ||||||||||||::::::|||||||||||||||||||.'||:|||||||
      51 HisProGlnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 67

     168 CTTGTATCAATCATGTGCCAGGCCCGGGGCAGGATATCGGATCCAGCAGT 217
         |||||||||||||||||||||||||||::|||||||||||||   |
      67 rLeuTyrAsnAspCysProGlyProGlyArgAspThrAspCysArgVaIC 84

     218 GTGACAGCCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGATCACTGCCTC 267
         ||      |||::::::|||||   |||||||||||||||:::|:.|||
      84 ysAlaProGlyThrTyrThrAlaLeuGluAsnHisLeuArgArgCysLeu 100

     268 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 317
         |||||||||:::||||||   ||||||   |||||||||||||||   ||
     101 SerCysSerArgCysArgAspGluMetProGlnValGluIleSerProCy 117

     318 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAATCAGTACCGGC 367
         :::|||||:|||||||||||||||||||||||||||||||:::|||||
     117 sValValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgG 134

     368 ATTATTGGAGTCAAAACCTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 417
         ::|||||::::|:|:::   |||:::|||:::|||||||||||||||
     134 luTyrTrpGlyGluThrGlyPheArgCysLeuAspCysSerLeuPro 150

     418 AATGGCACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCAC 467
         ||||||||||||:::::   |||||||||:::|||||||||||||:
     151 AsnGlyThrValAsnIleProCysGlnGluArgGlnAspThrIleCysHi 167

     468 CTGCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTA 517
         ||||||   ||||||||||||||:   :::|||::|||||   :
     167 sCysHisMetGlyPhePheLeuLysGlyAlaLysGluCysValSerCysHisA 184

     518 ACTGTAACAAAAGCCCTGCACTGCACGAACTTGTGCCTACCCCAGATTGAC 567
         ::|||||||||:::   ||||||   |||||||||      :::   :::
     184 spCysLysAsnLys...GluCysGluLysLeuCysProThrArgProSer 199

     568 AATGTTAAGGGCACTGAGGACTCAGCCACCACA 600
         :::   |||   :::::::::   |||||||||
     200 ThrGlyLysAspSerGlnAspProGlyThrThr 210

seq_name: SwissProt_39:TNRC_HUMAN

seq_documentation_block:
ID   TNRC_HUMAN     STANDARD;      PRT:   455 AA.
AC   P36941;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE   2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN   LTBR OR TNFCR OR TNFRSF3.
OS   Homo sapiens (Human).
OG   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93252381; PubMed=8486360;
RA   Baens M., Chatlanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT   "Construction and evaluation of a hncDNA library of human 12p
RT   transcribed sequences derived from a somatic cell hybrid.";
RL   Genomics 16:214-218(1993).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=94225209; PubMed=8171323;
RA   Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA   Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
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RT   "A lymphotoxin-beta-specific receptor.";
RL   Science 264:707-710(1994).
CC   -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC       IMMUNE DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L04270; AAA36757.1; -.
DR   HSSP; P25942; 1CDF.
DR   MIM; 600979; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     30       POTENTIAL.
FT   CHAIN       31    435       LYMPHOTOXIN-BETA RECEPTOR.
FT   DOMAIN      31    227       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   228    248       POTENTIAL.
FT   DOMAIN     249    435       CYTOPLASMIC (POTENTIAL)
FT   DOMAIN      42    211       4 X TNFR-CYS.
FT   REPEAT      42     81       TNFR CYS 1.
FT   REPEAT      82    124       TNFR-CYS 2.
FT   REPEAT     125    168       TNFR-CYS 3.
FT   REPEAT     169    211       TNFR-CYS 4.
FT   DISULFID    43     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     80       BY SIMILARITY.
FT   DISULFID    83     98       BY SIMILARITY.
FT   DISULFID   101    116       BY SIMILARITY.
FT   DISULFID   104    124       BY SIMILARITY.
FT   DISULFID   126    132       BY SIMILARITY.
FT   DISULFID   139    148       BY SIMILARITY.
FT   DISULFID   142    167       BY SIMILARITY
FT   DISULFID   170    185       BY SIMILARITY.
FT   CARBOHYD    40     40       N-LINKED (GLCNAC. . .) (POTENTIAL)
FT   CARBOHYD   177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   435 AA;  46709 MW;  624526E6022E656F CRC64;


alignment_scores:
            Quality:  213.50              Length:    214
              Ratio:  1.923                 Gaps:     11
 Percent Similarity:  51.869   Percent Identity: 30.841

alignment_block:
 US-09-525-998A-11 x TNRC_HUMAN  ..

 Align seq 1/1  to: TNRC_HUMAN  from: 1  to: 435

      33 GCCACTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTA 82
         ||||||:::|||||||||   :::   |||   :::   ||| |||:::
       6 AlaThrSerAlaProGlyLeuAlaTrpGlyProLeuValLeu.GlyLeuP 22

      83 TTGGA..... ..... 87
         ::|||
      22 heGlyLeuLeuAlaAlaSerGlnProGlnAlaValProProTyrAlaSer 38

      88 ...GATAGTGTGTGT......CCCCAAGCAAAATATATCCACCCTCAAAA 128
            ::::::::::|||        :::   :::|||   :::|||||||::
      39 GluAsnGlnThrCysArgAspGlnGluLysGluTyrTyrGlaProGlnHi 55

     129 TAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATG 178
         :::   ||||||||::::::|||      ||||||||||:::
      55 sArg...IleCysCysSerArgCysProProGlyThrTyrValSerAlaL 71

     179 ACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGC 228
         |||   :::      :::||||||   |||      |||   ::::::
      71 ysCys...SerArgIleArgAspThrValCysAlaThrCysAlaGluAsn 86

     229 TCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGGTCCAA 278
         ||:::::          |||:::|||      |||      |||
      87 SerTyrAsnGluHisTrpAsnTyrLeuThrIleCysGlnLeuCysArgPr 103

     279 ATGCCGAAAGGAAATGGGTCAGTGGAGATCTCTTCTTGCACAGTGGACC 328
         |||         ||||||      |||||||:::   ||||||      |
     103 oCysAspProValMetGlyLeuGluGluIleAlaProCysThrSerLysA 120

     329 GGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGT 378
         ||   |||   |||   |||...   ::::::::          |||:::
     120 rgLysThrGlnCysArgCysGlnProGlyMetPheCysAlaAlaTrpAla 136

     379 GAAAACCTTTTCCAGTGCTTCAATTGCAGCCTC.........TGCCTCAA 419
                    |||    ::|||:::|||        |||
     137 .........LeuGluCysThrHisCysGluLeuLeuSerAspCysProPr 150

     420 TGGGACCGTGCACCTCTCCTGCCAGGAG.....AAACAGAACACCGTGT 463
         ||||||              :::|||    |||   |||:::   |
     150 oGlyThrGluAlaGluLeuLysAspGluValGlyLysGlyAsnAsnHisC 167

     464 GCACC   TGCCATGCAGGTTTCTTCTAAGAGAAAACGAGTGTGTCTCC 510
         |||::   |||   ||||||   |||      :::|||
     167 ysValProCysLysAlaGlyHisPhe......GlnAsnThrSerSerPro 181

     511 TGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCA 560
         :::::.|||  .          ::|||  .          |||
     182 SerAlaArgCysGlnProHisThrArgCysGluAsnGlnGlyLeu..... 196

     561 GATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCACA 600
         :::|||   :::   ||||||   :::|||   ||||||
     197 .ValGluAlaAlaProGlyThrAlaGlnSerAspThrThr 209

seq_name: SwissProt_39:WSL1_HUMAN

seq_documentation_block:
ID   WSL1_HUMAN      STANDARD;      PRT;   417 AA.
AC   Q93038, Q93036, Q93037, Q92083, P78515, Q99831, Q99722, P78507;
AC   Q99830;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   WSL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS-
DE   MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)
DE   (APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED
DE   RECEPTOR OF DEATH) (LARD).
GN   TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.
RC   TISSUE=Lymphoid;
RX   MEDLINE=97088617; PubMed=8934525;
RA   Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
RA   Grinham C.J., Brown R., Farrow S.N.;
RT   "A death domain-containing receptor that mediates apoptosis.";
RL   Nature 384:372-375(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Umbilical vein endothelial cells;
RX   MEDLINE=97081063; PubMed=8875942;
RA   Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
RA   Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.,
RT   "Signal transduction by DR3, a death domain-containing receptor
RT   related to TNFR-1 and CD95.";
```

```
RL   Science 274:990-992(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=97148200; PubMed=8994832;
RA   Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
RA   Goddard A.D., Bauer K.D., Ashkenazi A.;
RT   "Apo-3, a new member of the tumor necrosis factor receptor family,
RT   contains a death domain and activates apoptosis and NF-kappa-B.";
RL   Curr. Biol. 6:1669-1676(1996).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97272273; PubMed=9114039;
RA   Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
RA   McMichael A.J., Bell J.I.;
RT   "LARD: a new lymphoid-specific death domain containing receptor
RT   regulated by alternative pre-mRNA splicing.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RN   [6]
RP   SEQUENCE OF 4-417 FROM N.A.
RC   TISSUE=Brain, and Fetal lung;
RX   MEDLINE=97205335; PubMed=9052839;
RA   Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
RA   Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
RA   Browning J.L., Macdonald H.R., Tschopp J.;
RT   "TRAMP, a novel apoptosis-mediating receptor with sequence homology
RT   to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
RL   Immunity 6:79-88(1997).
RN   [7]
RP   SEQUENCE OF 7-417 FROM N.A.
RC   TISSUE=Brain;
RA   Chaudhary P.M., Hood L.E.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INDUCES APOPTOSIS AND ACTIVATES NUCLEAR FACTOR KAPPA-B
CC       (NF-KAPPAB). DIRECTLY INTERACTS WITH TRADD ADAPTATOR MOLECULE. MAY
CC       PLAY A ROLE IN REGULATING LYMPHOCYTE HOMEOSTASIS.
CC   -!- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
CC       THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO
CC       ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; WSL-1/LARD-1A (SHOWN HERE),
CC       WSL-S1/LARD-3 AND WSL-S2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
CC       LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
CC       COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
CC   -!- PTM: GLYCOSYLATED (PROBABLE).
CC   -!- SIMILARITY: CONTAINS A LA-N&PR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y09392; CAA70561.1; -.
DR   EMBL; Y09392; CAA70559.1; -.
DR   EMBL; Y09392; CAA70560.1; -.
DR   EMBL; U72763; AAC50819.1; -.
DR   EMBL; U83599; AAB41434.1; -.
DR   EMBL; U83600; AAB41435.1; -.
DR   EMBL; U78029; AAB40918.1; -.
DR   EMBL; U74611; AAB39714.1; -.
DR   EMBL; U94501; AAC51806.1; -.
DR   EMBL; U94504; AAC51809.1; -.
DR   EMBL; U75380; AAC51192.1; -.
DR   EMBL; U75381; AAC51193.1; -.
DR   EMBL; U83597; AAB41432.1; -.
DR   HSSP; P19438; 1TNR.
DR   MIM; 603366; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   PROSITE; PS50052; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Apoptosis; Alternative splicing; Transmembrane; Signal;
KW   Repeat.
FT   SIGNAL       1     24       POTENTIAL.
FT   CHAIN       25    417       WSL-1 PROTEIN.
FT   DOMAIN      25    199       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   200    220       POTENTIAL.
FT   DOMAIN     221    417       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      34    192       4 X TNFR-CYS.
FT   REPEAT      34     71       TNFR-CYS 1.
FT   REPEAT      72    115       TNFR-CYS 2.
FT   REPEAT     116    163       TNFR-CYS 3.
FT   REPEAT     164    192       TNFR-CYS 4.
FT   DOMAIN     332    413       DEATH.
FT   CARBOHYD    67     67       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   106    106       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC   182    218       SILGSCPPPCAAVCSWPQMFWVQVLIAGLVVPLLLGA ->
FT                               VLGPGAPGWPCGPPEAWSHPILHIPPLLASQAPGYCR (IN
FT                               ISOFORM WSL-S1).
FT   VARSPLIC   219    417       MISSING (IN ISOFORM WSL-S1).
FT   VARSPLIC   200    253       MFWVQVLLAGLVVPLLLGAILIYIYRHCWPHKPLVIADEAG
FT                               MEALIPPPATHLS -> SRWCAGNAPGRTGMDRGEAGEGG
FT                               NHPTPTSCFQCSGSRCSWILALWSPSCLGPP (IN
FT                               ISOFORM WSL-S2).
FT   VARSPLIC   254    417       MISSING (IN ISOFORM WSL-S2).
FT   MUTAGEN    354    354       L->A: SUPPRESSES HOMODIMERIZATION, TNFR1
FT                               INTERACTION, AND APOPTOTIC INDUCTION.
FT   MUTAGEN    356    356       L->A: SUPPRESSES HOMODIMERIZATION, AND
FT                               TNFR1 INTERACTION.
FT   MUTAGEN    373    373       D->A: SUPPRESSES HOMODIMERIZATION, AND
FT                               TNFR1 INTERACTION.
FT   CONFLICT     4      6       RPR -> AAA (IN REF. 6).
FT   CONFLICT    60     60       P -> H (IN REF. 7).
FT   CONFLICT   167    167       P -> L (IN REF. 6 AND 7).
FT   CONFLICT   312    312       A -> R (IN REF. 1).
FT   CONFLICT   370    370       R -> L (IN REF. 1).
FT   CONFLICT   381    381       R -> H (IN REF. 1).
SQ   SEQUENCE   417 AA;  45385 MW;  5226319DFDB467U6 CRC64;


alignment_scores:
            Quality:  209.50              Length:     186
              Ratio:  2.054                 Gaps:       7
 Percent Similarity:  54.839   Percent Identity:  29.032

alignment_block:
 US-09-525-998A-11 x WSL1_HUMAN  ..

 Align seq 1/1  to: WSL1_HUMAN  from: 1  to: 417

      43 CTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTATTGGAGATAG 92
         ||||||   :::|||::::|||         :::|||         :::
      15 LeuLeuLeuValLeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerPr 61

      93 TGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTGGATTTGCT 142
            |||     :::      :::|||   :::   :::   :::||||
      62 oArgCysAspCysAlaGlyAspPheHisLysLysIleGlyLeuPheCysC 48

     143 GTACCAAGTGCCACAAAGGAACCTTACTTGTACAAIGACTGTGTCAGCCCG 192
         ||      |||     |||  ||||||     ***       |||
      48 ysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysLysGluPro 64

     193 GGGTAGGATACGGACTGTAGGGAGTGTGACAG***********AATGTTC 242
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```
                 :::::   |||     |||    ::     |||   |||
 65 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTr 81

243 AGAAAACCACCTCAGA . CACTGCCTCAGCTGCTCCAAATGCCGAAAGG 289
     ||||||||   :::      |||      |||      |||   ::::
 81 pGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluG 98

290 AAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTG 339
     ::  ::.||||||   ..          |||  ::::      |||:||
 98 nAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArg 114

340 TGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTT 389
     |||||||||:::   :::   :::                :::::
115 CysGlyCysLysProGlyTrpPheValGluCys .....   GlnValSe 128

390 CCAGTGC                TTCAATTGCAGCCTCTGCCTCAAT   G 421
     ||||||                |||   |||...   ||||||:::   |
128 rGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCysG 145

422 GGACCGTGCAC..      .    CTCTCCTGCCAGGAGAAACAGAACACC 459
     ||::::::|||              |||   |||::::::::   ...
145 lyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 161

460 GTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTC 509
             ||||||   ||||||            :::   |||||||
162 CysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSe 178

510 CTGT.......          AGTAACTGTAAGAAAAGCCTGGAGTGCACGA 544
     ||||                  ......|||   ...      ::||||:::
178 rCysProThrSerThrLeuGlySerCysProGlu......ArgCysAlaA 193

545 AGTTGTGC 552
       :::|||
193 laValCys 195
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seq_name: SwissProt_39:NGFR_HUMAN

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seq_documentation_block:
ID   NGFR_HUMAN      STANDARD;      PRT;   427 AA.
AC   P08138;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE   (GP80-LNGFR) (P75 ICD).
GN   NGFR OR TNFRSF16.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87051725; PubMed=3022937;
RA   Johnson D., Lanahan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
RA   Bothwell M., Chao M.;
RT   "Expression and structure of the human NGF receptor.";
RL   Cell 47:545-554(1986).
RN   [2]
RP   SEQUENCE OF 1-22 FROM N.A.
RX   MEDLINE=89096903; PubMed=2850481;
RA   Sehgal A., Patil N., Chao M.;
RT   "A constitutive promoter directs expression of the nerve growth factor
RT   receptor gene.";
RL   Mol. Cell. Biol. 8:3160-3167(1988).
CC   -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC       NT-3, AND NT-4.
CC   -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC       BOND FORMATION.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M14764; AAB59544.1; -.
DR   EMBL; M21621; AAA36363.1; -.
DR   PIR; A25218; GQHUN.
DR   HSSP; P07174; 1NGR.
DR   MIM; 162010; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW   Phosphorylation; Signal
FT   SIGNAL        1     28
FT   CHAIN        29    427       LOW-AFFINITY NERVE GROWTH FACTOR
FT                                RECEPTOR.
FT   DOMAIN       29    250       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    251    272       POTENTIAL.
FT   DOMAIN      273    427       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       31    189       4 X TNFR-CYS.
FT   REPEAT       31     65       TNFR-CYS 1.
FT   REPEAT       66    107       TNFR-CYS 2.
FT   REPEAT      108    147       TNFR-CYS 3.
FT   REPEAT      148    189       TNFR-CYS 4.
FT   DOMAIN      344    421       DEATH.
FT   DISULFID     32     43       BY SIMILARITY.
FT   DISULFID     44     57       BY SIMILARITY.
FT   DISULFID     47     64       BY SIMILARITY.
FT   DISULFID     67     83       BY SIMILARITY.
FT   DISULFID     86     99       BY SIMILARITY.
FT   DISULFID     89    107       BY SIMILARITY.
FT   DISULFID    109    122       BY SIMILARITY.
FT   DISULFID    125    138       BY SIMILARITY.
FT   DISULFID    128    146       BY SIMILARITY.
FT   DISULFID    149    164       BY SIMILARITY.
FT   DISULFID    167    180       BY SIMILARITY.
FT   DISULFID    170    188       BY SIMILARITY.
FT   DOMAIN      197    248       SER/THR-RICH.
FT   CARBOHYD     60     60       N-LINKED (GLCNAC   ) (POTENTIAL).
SQ   SEQUENCE   427 AA;  45183 MW;  B09FA143FB3D625B CRC64;
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alignment_scores:
          Quality:  207.50             Length:    194
            Ratio:  1.921                Gaps:     12
 Percent Similarity: 55.670   Percent Identity: 31.443

alignment_block:
 US-09-525-998A-11 x NGFR_HUMAN

 Align seq 1/1  to: NGFR_HUMAN  from: 1  to: 427

  34 CCACTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTAT 83
      |||   :..||||||   ||||||  .:|||.:        .   |||
  13 ProArgLeuLeuLeuLeuLeuLeuLeuGlyValSerLeuGlyGly..... 27

  84 TGGAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATT 133
           .   .  ||||||   |||   |||   |||           ::::
  28 .AlaLysGluAlaCysProThrGlyLeuTyrThrHis          SerG 41

 134 CGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGT 183
        .   ||||||       |||       |||       ...   :::   |||
```

```
      41 lyGluCysCysLysAlaCysAsnLeuGlyGluGlyValAlaGlnProCys 57

     184 CCAGCCCCCGCCCAGGATACCGACTGCACCCAGTGC  CACAGCCGCTC 230
         |||   ...|||   |||   |||...   |||   ...|||   ...
      58 ...GlyAlaAsnGln...ThrValCysGluProCysLeuAspSerValTh 72

     231 CTTCACCGCTTCAGAAAACACACTCAGACACTGCCTCAGTTGTCTAAAT 280
         .|||...      ...          |||      |||.....  |
      72 rPheSerAspValValSerAlaThrGluProCysLysProCysThrGluC 89

     281 CCCCAAAGCAAATGCCTCACCTCCAGAATCTCCTCCT..TCCACACTGCAC 327
         ||         :..|||      .:...:|||...   |||...
      89 ys       ...ValGlyLeuGlnSerMetSerAlaProCysValGluAla 102

     328 CCCCACACCCTCTCTCCCTCCAGGAACAACCACTACCGCATCATCCAG 377
         |||...||||||   |||            |||   .. |||    .
     103 AspAspAlaValCysArgCys.        AlaTyrGlyTyrTyrGlnAs 116

     378 TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACC  426
         :|||:::        |||      |||    .  |||      |||
     116 pGluThrThrGlyArgCysGluAlaCysArgValCysGluAlaGlySerG 133

     427 . CTGCAGCTCTCCTGCCAGGAGAAACAGAACACCCTGCTCC ..ACCTGC 471
           :::   :::||||||||||:::|||||||||||||||||      |||
     133 lyLeuValPheSerCysGlnAspLysGlnAsnThrValCysGluGluCys 149

     472 CATGCAGGTTTCTTTCTAAGAGAA ...          AACGAGTGTGTCTC 509
             |||   :::      |||              :::   ||||:::
     150 ProAspGlyThrTyrSerAspGluAlaAsnHisValAspProCysLeuPr 166

     510 CTGTAGTAACTGT.  .      . AAGAAAAGCTGGAGTGCAGAAGT 547
          |||:::   |||            ......      ||||||||||...
     166 oCysThrValCysGluAspThrGluArgGlnLeuArgGluCysThrArgT 183

     548 TGTGCCTACCCCAGATTGAGAATGTTAAGCCC 579
         ...      ...  |||.....:  |||
     183 rpAlaAspAlaGluCysGluGluIleProGly 193

seq_name. SwissProt_39:NGFR_RAT

seq_documentation_block:
ID   NGFR_RAT       STANDARD;      PRT:   425 AA.
AC   P07174;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE   (GP80-LNGFR) (P75 ICD).
GN   NGFR.
OS   Rattus norvegicus (Rat).
OC   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
OC   Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Rattus
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87115859; PubMed=3027580;
RA   Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
RT   "Gene transfer and molecular cloning of the rat nerve growth factor
RT   receptor.",
RL   Nature 325:593-597(1987).
RN   [2]
RP   SEQUENCE OF 1-22 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93077038; PubMed=1446821;
RA   Metsis M., Timmusk T., Arumae U., Saarma M., Persson H.;
RT   "Regulatory elements and transcriptional regulation by testosterone
RT   and retinoic acid of the rat nerve growth factor receptor promoter";
RL   Gene 121:247-254(1992).
RN   [3]
RP   STRUCTURE BY NMR OF 334-418.
RX   MEDLINE=97449145; PubMed=9305641;
RA   Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.;
RT   "NMR structure of the death domain of the p75 neurotrophin receptor.";
RL   EMBO J. 16:4999-5005(1997).
CC   -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC       NT-3, AND NT-4.
CC   -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC       BOND FORMATION.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/INFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X05137; CAA28783.1; -.
DR   EMBL; X61269; -; NOT_ANNOTATED_CDS.
DR   PIR; A26431; A26431.
DR   PDB; 1NGR; 29-JUL-97.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW   Phosphorylation; Signal; 3D-structure.
FT   SIGNAL       1     29
FT   CHAIN       30    425       LOW-AFFINITY NERVE GROWTH FACTOR
FT                                 RECEPTOR.
FT   DOMAIN       30    251       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    252    273       POTENTIAL.
FT   DOMAIN      274    425       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       32    190       4 X INFR CYS.
FT   REPEAT       42     66       TNFR-CYS 1.
FT   REPEAT       67    108       TNFR CYS 2.
FT   REPEAT      109    148       TNFR-CYS 3.
FT   REPEAT      149    190       TNFR CYS 4.
FT   DOMAIN      198    249       SER/THR-RICH.
FT   DOMAIN      354    419       DEATH.
FT   DISULFID     33     44       BY SIMILARITY.
FT   DISULFID     45     58       BY SIMILARITY.
FT   DISULFID     48     65       BY SIMILARITY.
FT   DISULFID     68     84       BY SIMILARITY.
FT   DISULFID     87    100       BY SIMILARITY.
FT   DISULFID     90    108       BY SIMILARITY.
FT   DISULFID    110    123       BY SIMILARITY.
FT   DISULFID    126    139       BY SIMILARITY.
FT   DISULFID    129    147       BY SIMILARITY.
FT   DISULFID    150    165       BY SIMILARITY.
FT   DISULFID    168    181       BY SIMILARITY.
FT   DISULFID    171    189       BY SIMILARITY.
FT   CARBOHYD     67     67       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     71     71       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   425 AA;  45492 MW;  B2E152D9423827F8 CRC64;


alignment_scores:
            Quality:  793.50              Length:    192
              Ratio:    4.825               Gaps:     12
 Percent Similarity:   55.208   Percent Identity:   29.208

alignment_block:
 US-09-525-998A-11 x NGFR_RAT   ..

 Align seq 1/1  to: NGFR_RAT  from: 1  to: 425
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 40 GTGGTCCTGGAGCTGTTGGTGGCAATATACCCCTCAGGGGTTATTGGAGA 89
    :::|||||   |||::::::|||::      :  |||      :::
 16 LeuLeuLeuLeuLeuIleLeuGlyValSerSerGlyGly     AlaLy 30

 90 TAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATTT 139
     :::::|||      |||   |||   |||         ::::::   |
 30 sGluThrCysSerThrGlyLeuTyrThrHis.........SerGlyGluC 44

140 GCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTGCCAGGC 189
    ||||      |||::.  |||     ::   ...   |||   |||
 44 ysCysLysAlaCysAsnLeuGlyGluGlyValAlaGlnProCys   Gly 59

190 CCGGGGCAGGATACGGACTGCAGGGAGTGT   GAGAGCGGCTCCTTCAC 236
     :  |||   |||   |||   :   |||                 |||:
 60 AlaAsnGln...ThrValCysGlnProCysLeuAspAsnValThrPheSe 75

237 CGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAA 286
    :          :::            |||      |||      |||
 75 rAspValValSerAlaThrGluProCysLysProCysThrGluCys     90

287 AGGAAATGGGTCAGGTGGAGATCTCTTCT   TGCACAGTGGACCGGGAC 333
       :::|||      ::::::|||:::   ||||:            |||
 91  ....LeuGlyLeuGlnSerMetSerAlaProCysValGluAlaAspAsp 105

334 ACCGTGTGTGGCTGCAGGAACAACCAGTACCGGCATTATTGGAGTGAAAA 383
    :::|||||   |||            |||   ...|||   ...|||.:
106 AlaValCysArgCys         AlaTyrGlyTyrTyrGlnAspGluGl 119

384 CCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACC...GTGC 430
          :::|||      ||||||:::|||      |||:::   :::
119 uThrGlyHisCysGluAlaCysSerValCysGluValGlySerGlyLeuV 136

431 ACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGC  ACTTGCCATGCA 477
      :::||||||||||:::|||||||||||||||||      |||
136 alPheSerCysGlnAspLysGlnAsnThrValCysGluGluCysProGlu 152

478 GGTTTCTTTCTAAGAGAA... .........AACGAGTGTGTCTCCTGTAG 515
     ||   :::     |||              :::   |||:::   |||::
153 GlyThrTyrSerAspGluAlaAsnHisValAspProCysLeuProCysTh 169

516 TAACTGT.....       AAGAAAAGCCTGGAGTGCACGAAGTTGTGCC 553
     :   |||            ::::::      |||||||||      :::
169 rValCysGluAspThrGluArgGlnLeuArgGluCysThrProTrpAlaA 186

554 TACCCCAGATTGAGAATGTTAAGGGC 579
          :::   |||:::::   :||
186 spAlaGluCysGluGluIleProGly 194
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seq_name: SwissProt_39:VT2_SFVKA

seq_documentation_block:
ID   VT2_SFVKA      STANDARD;      PRT;   325 AA.
AC   P25943;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2)
GN   T2.
OS   Shope fibroma virus (strain Kasza) (SFV)
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Leporipoxvirus.
OX   NCBI_TaxID=10272;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87321103; PubMed=2820128;
RA   Upton C., Delange A.M., McFadden G.;
RT   "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RT   telomeric region of the Shope fibroma virus genome.";
RL   Virology 160:20-30(1987).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=91207415; PubMed=1850261;
RA   Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA   McFadden G., Goodwin R.G.;
RT   "T2 open reading frame from the Shope fibroma virus encodes a soluble
RT   form of the TNF receptor.";
RL   Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC   -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC       REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC       ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M17433; -; NOT_ANNOTATED_CDS.
DR   EMBL; A23727; CAA01687.1; -.
DR   PIR; B43692; B43692.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    325       TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT   DOMAIN       27    186       4 X TNFR-CYS.
FT   REPEAT       27     62       TNFR-CYS 1.
FT   REPEAT       63    104       TNFR-CYS 2.
FT   REPEAT      105    147       TNFR-CYS 3.
FT   REPEAT      148    186       TNFR-CYS 4.
FT   CARBOHYD    105    105       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    181    181       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    205    205       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    238    238       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   325 AA;  35132 MW;  8105B0339198A71E CRC64;
```

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alignment_scores:
           Quality:  190.50            Length:    203
             Ratio:  1.832               Gaps:     11
 Percent Similarity:  51.232   Percent Identity: 29.064

alignment_block:
 US-09-525-998A-11 x VT2_SFVKA   ..

 Align seq 1/1  to: VT2_SFVKA  from: 1  to: 325

  25 CTGCTGCTGCTCACTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTC 74
     :: |||      :::: ||||||       ||||      ||||
   1 MetLeuArgLeuIleAlaLeuLeuValCysValValTyrValTyr..... 15

  75 AGGGGTTATTGGAGATAGTGTG  ....   TGTGCCCAAGGAAAA     111
               ||||||:::|||           |||||||||
  16  .....  GlyAspAspValProTyrSerSerAsnGlnGlyLysCysG 29

 112 ..........TATATCCACCCTCAAAATAATTCGATTTGCTGTACCAAG 150
               |||          ..............||||||......
  29 lyGlyHisAspTyr.........GluLysAspGlyLeuCysCysAlaSer 42

 151 TGCCACAAAGGAACCTACTTGTACAATGACTGTGCCAGGCCGGGGCAGGA 200
     ||||||   |||   |||      :::   |||   |||||||||  ::
  43 CysHisProGlyPheTyrAlaSerArgLeuCys...GlyProGlySerAs 58

 201 TACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACC 250
     :|||   |||      ||||||:::|||::||||||||||||   ||||
  58 nThrValCysSerProCysGluAspGlyThrPheThrAlaSerThrAsnH 75

 251 ACCTCAGACACTGCCTCAGCTGC  TCCAAATGCCGAAAGGAAATGGGT 297
```

```
         ||           |||:::||||||   :::   |||      :::::::::
  75 isAlaProAlaCysValSerCysArgGlyProCysThrGlyHisLeuSer 91

 298 CAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTG 347
          |||   :::   |||          :::|||   ||||||:::||
  92    ..GluSerGlnProCysAspArgThrHisAspArgValCysAsnCy 106

 348 CAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAACCTTTTCCAGTCCT 397
      |       :::::|||             :::::|||
 106 sSerThrGlyAsnTyrCysLeuLeuLysGlyGlnAsn............. 118

 398 TCAATTGCAGCCTCTGCCTCAATGGCACCGTGCACCTCTCCTGCCAGCAG 447
        :::|||   :::|||          |||
 119   GlyCysArgIleCysAlaProGlnThr..................... 127

 448 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAA 497
                          |||   |||||:::   :::     ::
 128 ..................LysCysProAlaGlyTyrGlyValSerGlyHi 138

 498 CGAGTGTGTCTCCTGTAGTAACTGTAAGAAAAGCCTGGAGTGCACGAAGT 547
     :        ::::::   :::   ||:::|||
 138 sThrArgAlaGlyAspThrLeuCysGluLys................... 148

 548 TGTGCCTACCCCAGATT....GACAATCTTAAGGGCACTGAGGACTCA 591
        |||   |||:::           ::::::::::::   ||||||
 149 ..CysProProHisThrTyrSerAspSerLeuSerProThrGluArgCys 164

 592 GGCACCACA 600
     |||||:::
 165 GlyThrSer 167
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seq_name: SwissProt_39:VT2_MYXVL

seq_documentation_block:

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ID   VT2_MYXVL      STANDARD;      PRT;   326 AA.
AC   P29825;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN   T2.
OS   Myxoma virus (strain Lausanne).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Leporipoxvirus.
OX   NCBI_TaxID=31530;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91335768; PubMed=1651597;
RA   Upton C., Macen J.L., Schreiber M., McFadden G.;
RT   "Myxoma virus expresses a secreted protein with homology to the tumor
RT   necrosis factor receptor gene family that contributes to viral
RT   virulence.";
RL   Virology 184:370-382(1991).
CC   -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC       REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC       ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M95181; AAA46632.1; -.
DR   EMBL; A23729; CAA01688.1; -.
DR   PIR; A40566; GQVZML.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    326       TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT   DOMAIN       27    186       4 X TNFR-CYS.
FT   REPEAT       27     62       TNFR-CYS 1.
FT   REPEAT       63    104       TNFR-CYS 2.
FT   REPEAT      105    147       TNFR-CYS 3.
FT   REPEAT      148    186       TNFR-CYS 4.
FT   CARBOHYD     66     66       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    181    181       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    2[illegible]    2[illegible]       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    238    238       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   326 AA;  35208 MW;  ABBF027E347252FF CRC64;
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alignment_scores:

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          Quality:   187.50             Length:     232
            Ratio:   1.659                Gaps:       9
Percent Similarity:  48.707   Percent Identity:  2[illegible]
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alignment_block:

US-09-525-998A-11 x VT2_MYXVL ..

Align seq 1/1 to: VT2_MYXVL from: 1 to: 326

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  40 GTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTT........ 81
     :::|||||||        ::::::    :::|||    :::|||:::
   6 LeuLeuLeuAlaTyrValAlaCysValTyrGlyGlyGlyAlaProTyrGl 22

  82 .ATTGGAGATAGTGTGTGTCCCCAAGGAAAATATATCAA[illegible]AAAATA 130
              :::    |||       :::    |||           ::::::::
  22 yAlaAspArg[illegible]..........GluLysA 36

 131 ATTCGATTTGCTGTACCAAGTGCCACAAACCAACCTACTTGTACAATGAC 180
     :::::::::||||||||||:::|||         |||:::|||      :::
  36 spGlyLeuCysCysThrSerCysProProGlySerTyrAlaSerArgLeu 52

 181 TGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTC 230
     |||    |||:::|||:::||||||    |||        |||::::::   ::
  53 Cys...GlyProGlySerAspThrValCysSerProCysLysAsnGluTh 68

 231 CTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGC...TCCA 277
     :||||||||||||    ||||||              |||:::||||||   ::::
  68 rPheThrAlaSerThrAsnHisAlaProAlaCysValSerCysArgGlyA 85

 278 AATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTCCACACTCCAC 327
     :::|||          ::::::::::           |||    ::::||||||.
  85 [illegible]Thr 99

 328 CGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTAC.............. 363
     ||||||    ||||||    |||            :::::|||
 100 ArgAspArgValCysAspCysSerAlaGlyAsnTyrCysLeuLeuLysGl 116

 363 .................................................. 363

 116 yGlnGluGlyCysArgIleCysAlaProLysThrLysCysProAlaGlyT 133

 363 .................................................. 363

 133 yrGlyValSerGlyHisThrArgThrGlyAspValLeuCysThrLysCys 149

 364 ...CGGCATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCT 410
          |||:::    :::|||:::    :::    :::          :::|   :::
 150 ProArgTyrThrTyrSerAspAlaValSerSerThrGluThrCysThrSe 166

 411 CTGCCTCAATGGG...ACCGTGCACCTCTCCTGCCAGGAGAAACAGAACA 457
          :::|||       :::|||::::::::::                 :::::::|
 166 rSerPheAsnTyrIleSerValGluPheAsnLeuTyrProValAsnAspT 183

 458 CCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTC 507
```

```
      ||   ||||||      ||||||              ||||||   |||
  183 hrSerCysThrThrThrAlaGly            ProAsnGluValVal 195

  508 TCCTGTAGTAACTGTAAGAAAAGCCTG          GAGTGCACGAAGTT 548
      :::   |||:::   :::   ::|||          .:|||      ..
  196 LysThrSerGluPheSerValThrLeuAsnHisThrAspCysAspProVa 242

  549 GTGCCTACCCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGC 594
      :         :::      ::::::::::|||:::|||   :::|||
  212 lPheHisThrGlyTyrTyrGlyThrSerGlySerCysGlyAlaGly 227

seq_name: SwissProt_39:TNR2_MOUSE

seq_documentation_block:
ID   TNR2_MOUSE     STANDARD;      PRT;   474 AA.
AC   P25119; P97893;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
GN   TNFRSF1B OR TNFR2 OR TNFR 2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246168; PubMed=1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE OF 1-26 FROM N.A.
RC   STRAIN=NOD;
RA   Jacob C.O., Liu J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-22 FROM N.A.
RC   TISSUE=Liver;
RA   Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60469; AAA39752.1; -.
DR   EMBL; M59378; AAA40463.1; -.
DR   EMBL; U39488; AAA85021.1; -.
DR   EMBL; X87128; CAA60618.1; -.
DR   PIR; B38634; B38634.
DR   HSSP; P19438; 1NCF.
DR   MGD; MGI:1314883; Tnfrsf1b.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam, PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    474       TUMOR NECROSIS FACTOR RECEPTOR 2.
FT   DOMAIN       23    258       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    259    288       POTENTIAL.
FT   DOMAIN      289    474       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       39    203       4 X TNFR-CYS.
FT   REPEAT       39     77       TNFR-CYS 1.
FT   REPEAT       78    119       TNFR-CYS 2.
FT   REPEAT      120    164       TNFR-CYS 3.
FT   REPEAT      165    203       TNFR-CYS 4.
FT   DISULFID     40     54       BY SIMILARITY.
FT   DISULFID     55     68       BY SIMILARITY.
FT   DISULFID     58     76       BY SIMILARITY.
FT   DISULFID     79     94       BY SIMILARITY.
FT   DISULFID     97    111       BY SIMILARITY.
FT   DISULFID    101    119       BY SIMILARITY.
FT   DISULFID    121    127       BY SIMILARITY.
FT   DISULFID    136    145       BY SIMILARITY.
FT   DISULFID    139    163       BY SIMILARITY.
FT   DISULFID    166    181       BY SIMILARITY.
FT   CARBOHYD     69     69       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    195    195       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   474 AA;  50319 MW;  462FAF398C410563 CRC64;


alignment_scores:
           Quality:  181.00              Length:    161
             Ratio:  1.946                 Gaps:      8
 Percent Similarity:  57.764   Percent Identity: 31.677

alignment_block:
 US-09-525-998A-11 x TNR2_MOUSE   ..

 Align seq 1/1  to: TNR2_MOUSE  from: 1  to: 474

   97 TGTCCCCAAGAAATATATCCACCCTCAAAATAATTCGATTTGCTGTAC 146
      |||      ::::::      :::   ::::::   ::::::::::::::
   40 CysGlnIleSerGlnGluTyrTyrAspArgLysAlaGlnMetCysCysAl 56

  147 CAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGC 196
      :||||||      |||   |||:::   :::   |||   :::      :
   56 alysCysProProGlyGlnTyrValTyrHisPheCys...AsnLysThrS 72

  197 AGGATACGGACTGCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAA 246
      :.||||||   |||   ::.|||||.:....   .::|||
   72 erAspThrValCysAlaAspCysGluAlaSerMetTyrThrGlnValTrp 88

  247 AACCACCTCAGACACTGCCTCAGCTGC...TCCAAATGCCGAAACGAAAT 293
      |||.....:|||   ||||||||||||   |||::|||      :::
   89 AsnGlnPheArgThrCysLeuSerCysSerSerSerCysThrThrAsp.. 104

  294 GGGTCAGGTGGAGATCTCTTCTTGCAGAGTGGACCCGGACACCGTGTGTG 343
      ||||||||||||   :::|||||   :::::::::   ||||||:
  105   ..GlnValGluIleArgAlaCysThrLysGlnGlnAsnArgValCysA 120

  344 GCTGCAGGAAGAACCAGTAC             CGGCATTATTGGAGTGAA 381
      ..|||.      :|||                 |||       |||
  120 laCysGluAlaGlyArgTyrCysAlaLeuLysThrHis......SerGly 134

  382 AACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGG...ACCGT 428
      :::      ||||||:::::   |||   |||      |||      ||
  135 SerCysArgGlnCysMetArgLeuSerLysCysGlyProGlyPheGlyVa 151

  429 GCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGC...ACCTGCCATG 475
      |    |||      :::   ||||::::::|||   :::|||
  151 lAlaSerSerArgAlaProAsnGlyAsnValLeuCysLysAlaCysAlaP 168

  476 CAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAACTGTAAG 525
```

```
         |||   |||       ::::::           |||   :::   |||:::
     168 roGlyThrPhe......SerAspThrThrSerSerThrAspValCysArg 182

     526 AAAAGCCTGGAGTGCACGAAGTTGTGCCTACCC 558
                        |||:::   |||::::::|||
     183 ProHisArgIleCysSerIleLeuAlaIlePro 193

seq_name: SwissProt_39:TNRC_MOUSE

seq_documentation_block:
ID   TNRC_MOUSE     STANDARD;      PRT;   415 AA.
AC   P50284;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN   LTBR OR TNFCR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CVB; TISSUE=Lung;
RX   MEDLINE=96072804; PubMed=7594541;
RA   Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA   Browning J.L., Ware C.F.;
RT   "Mouse lymphotoxin beta receptor. Molecular genetics, ligand binding,
RT   and expression.";
RL   J. Immunol. 155:5280-5288(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96163885; PubMed=8586432;
RA   Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA   Honjo T.;
RT   "The murine lymphotoxin beta receptor cDNA: isolation by the signal
RT   sequence trap and chromosomal mapping.";
RL   Genomics 30:312-319(1995).
CC   -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC       IMMUNE DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U29173; AAA68964.1; -.
DR   EMBL; L38423; AAB00846.1; -.
DR   EMBL; U30798; AAA81334.1; -.
DR   HSSP; P25942; 1CDF.
DR   MGD; MGI:104875; Ltbr.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    415       LYMPHOTOXIN-BETA RECEPTOR.
FT   DOMAIN       31    223       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    224    244       POTENTIAL.
FT   DOMAIN      245    415       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    213       4 X TNFR-CYS.
FT   REPEAT       42     81       TNFR-CYS 1.
FT   REPEAT       82    124       TNFR-CYS 2.
FT   REPEAT      125    170       TNFR-CYS 3.
FT   REPEAT      171    213       TNFR-CYS 4.
FT   DISULFID     43     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     80       BY SIMILARITY.
FT   DISULFID     83     98       BY SIMILARITY.
FT   DISULFID    101    116       BY SIMILARITY.
FT   DISULFID    104    124       BY SIMILARITY.
FT   DISULFID    126    132       BY SIMILARITY.
FT   DISULFID    139    150       BY SIMILARITY.
FT   DISULFID    142    169       BY SIMILARITY.
FT   DISULFID    172    187       BY SIMILARITY.
FT   CARBOHYD     40     40       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   415 AA;  44956 MW;  29B326A566AFF661 CRC64;

alignment_scores:
            Quality:  190.00              Length:     211
              Ratio:  1.714                 Gaps:       9
 Percent Similarity:  19.763    Percent Identity:  28.916

alignment_block:
 US-09-525-998A-11 x TNRC_MOUSE   ..

 Align seg 1/1  to: TNRC_MOUSE  from: 1  to: 415

       4 CCCCTCTTCACTGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTGGAGCT 53
         ||||||:::        |||            |||   |||   :||         ||
      11 GlyLeuAlaTrpGlyPro.........LeuLeuLeuGlyLeuSerGlyLe 24

      54 GTTGGTGGGAATATACCCCTCAGGGGTT............ATTGGAGATA 91
         ||||||:::         ||:::   |||                |||   ::::
      24 uLeuValAlaSerGlnProGlnLeuValProProTyrArgIleGluAsnG 41

      92 GTGTGTGT...CCCCAAGGAAAATATATCCACCCTCAAAATAATTCGATT 138
         ::::::|||          |||    |||         :::          :::::::::
      41 lnThrCysTrpAspGlnAspLysGluTyrTyrGluProMetHisAspVal 57

     139 TGCTGTACCAACTGCCACAAAGGAACCTACTTGTACAATCACTGTCCAGG 188
         ||||||:::::::|||          |||   :::::::::          |||   ::
      58 CysCysSerArgCysProProGlyGluPheValPheAlaValCys...Se 73

     189 CCCGCCCCAGGATACGGACTCCACCCACTCTCACAGCCCTTCCTTCACCC 238
         :    ::::|||||||||   |||:::    |||          ::::|||:::::
      73 rArgSerGlnAspThrValCys...ThrCysProHisAsnSerTyrAsnG 90

     239 CTTCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATCCCGAAAG 288
                   ||||| |||         |||         |||         :::
      90 luHisTrpAsnHisLeuSerThrCysGlnLeuCysArgProCysAspIle 106

     289 GAAATGGCTCAGCTGGAGATCTCTTCTTGCACACTGGACCCGGACC..CT 338
            :::|||         |||::::::   ||||||    ||||||     :::
     107 ValLeuGlyPheGluGluValAlaProCysThrSerAspArgLysAlaGl 123

     339 GTGTGCCTGCAGGAAGAACCAGTACCGGCATTATTGCACTGAAAACCTTT 388
          |||     |||:::    ::::::               |||    ::::::
     123 uCysArgCysGlnProGlyMetSerCysValTyrLeuAspAsn.....  137

     389 TCCAGTGCTTCAATTGCAGC................CTCTGCCTCAATGCG 423
           :::|||    :::|||:::                  ||||||       |||
     138 ..GluCysValHisCysGluGluGluArgLeuValLeuCysGlnProGly 153

     424 ACCCTCCACCTCTCCTCCCACGAGAAACAGAACACC..........GTGTG 464
         |||                     :::|||    :::::::|||
     154 ThrGluAlaGluValThrAspGluIleMetAspThrAspValAsnCysVa 170

     465 CACCTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTCTCTCCTCTA 514
             |||        |||    |||        :::|||                :
     170 lProCysLysProGlyHisPhe......GlnAsnThrSerSerProArgA 185

     515 GTAACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATT 564
         ::::::|||:::            ::::|||                       :::
     185 laArgCysGlnProHisThrArgCysGluIleGlnGlyLeu......Val 199
```

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     565 GAGAATGTTAAGGGCACTGAGGACTCAGGCACC 597
         |||   :::   |||||||:::   |||   |||
     200 GluAlaAlaProGlyThrSerTyrSerAspThr 210

seq_name: SwissProt_39:FASA_PIG

seq_documentation_block:
ID   FASA_PIG       STANDARD;      PRT;   332 AA.
AC   O77736;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE   (APO-1 ANTIGEN) (CD95).
GN   TNFRSF6 OR APT1 OR FAS.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hartinq B., Hoffmann I., Holtz J., Schulz R., Heusch G., Darmer D.;
RT   "Expression of apoptosis associated genes in hibernating and stunned
RT   myocardium of piq.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC       ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC       RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC       SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC       ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC       CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC       APOPTOSIS. FAS MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC       INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC       SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC    !  DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ001202; CAA04596.1; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    332       FASL RECEPTOR.
FT   DOMAIN       17    175       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    176    192       POTENTIAL.
FT   DOMAIN      193    332       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       45    164       3 X TNFR-CYS.
FT   REPEAT       45     81       TNFR-CYS 1
FT   REPEAT       82    125       TNFR-CYS 2
FT   REPEAT      126    164       TNFR-CYS 3.
FT   DOMAIN      227    311       DEATH.
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    116    116       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   332 AA;  37592 MW;  5BBB0368275ERDIB CRC64;

alignment_scores:
           Quality:  176.50              Length:    127
             Ratio:  2.418                 Gaps:      4
 Percent Similarity:  57.480   Percent Identity: 29.134

alignment_block:
 US-09-525-998A-11 x FASA_PIG   ..

 Align seq 1/1  to: FASA_PIG  from: 1  to: 332

      88 GATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTCGAT 137
         ...|||   |||||...|||.....          ..............
      43 GluSerGluCysProGluGlyGlnHis    .    ArgGluGlyGlnPh 56

     138 TTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAG 187
         :||||||     |||     |||         :::   ||||||   :
      56 eCysCysGlnProCysProProGlyLysArgLysHisAlaAspCysThrS 73

     188 GCCCGGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGC..TCCTTC 234
         :.|||||         ...|||     |||:::::::|||   ::::::
      73 erProGlyGlyAlaProGlnCysValProCysSerGluGlyGluAspTyr 89

     235 ACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCG 284
         |||   ::::::::|||         |||     |||     |||
      90 ThrAspLysAsnHisHisSerSerLysCysArgArgCysArgValCysAs 106

     285 AAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGACCGGGACA 334
         |||   |||           ..    ||||||       ::::::
     106 pGlyGluHisGlyLeuGluValGluLysAsnCysThrArgThrGlnAsnT 123

     335 CCGTGTGTGGCTGCAGGAAGAACCAGTACCGGCATTATTGGAGTGAAAAC 384
         ||   |||   |||::   |||   :::   |||       :::::::::
     123 hrLysCysArgCysLysProAsnPhePheCysHis......ThrSerGln 137

     385 CTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGCACCT 434
             ...|||      |||...   |||   ...|||.........
     138 CysGluHisCysAsnProCysThrThrCysGluHisGlyValIleGlu.. 153

     435 CTCCTGCCAGGAGAAACAGAACACCGTGTGC 465
         ...|||         ...||||||   |||
     154 .AsnCysThrProThrSerAsnThrLysCys 163

seq_name: SwissProt_49:CD40_BOVIN

seq_documentation_block:
ID   CD40_BOVIN     STANDARD;      PRT;   269 AA.
AC   Q28203;
DT   01-NOV 1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
GN   TNFRSF5 OR CD40.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 97281252; PubMed=9135560;
RA   Hirano A., Brown W.C., Estes D.M.;
RT   "Cloning, expression and biological function of the bovine CD40
RT   homologue: role in B-lymphocyte growth and differentiation in
RT   cattle.";
RL   Immunology 90:294-300(1997).
CC   -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC    !  SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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DR   EMBL; U57745; AAC48710.1; -.
DR   HSSP; P25942; 1CDF.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20   >269       CD40L RECEPTOR.
FT   DOMAIN       20    193       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    194    215       POTENTIAL.
FT   DOMAIN      216   >269       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       25    187       4 X TNFR-CYS.
FT   REPEAT       25     60       TNFR-CYS 1.
FT   REPEAT       61    103       TNFR-CYS 2.
FT   REPEAT      104    144       TNFR-CYS 3.
FT   REPEAT      145    187       TNFR-CYS 4.
FT   CARBOHYD    153    153       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     269    269
SQ   SEQUENCE   269 AA;  29983 MW;  746903F30F95F387 CRC64;


alignment_scores:
           Quality:  173.00            Length:    187
             Ratio:  1.648               Gaps:      7
 Percent Similarity:  56.150   Percent Identity: 29.947

alignment_block:
 US-09-525-998A-11 x CD40_BOVIN   ..

 Align seq 1/1  to: CD40_BOVIN  from: 1  to: 269

      28 CTGCTGCCACTGGTGCTCCTGGAGCTGTTGGTGGGAATATACCCCTCAGG 77
          ::::::   |||   |||       |||:::   |||::::::   :::::
       1 MetValArgLeuProLeuGlnCysLeuPheTrpGlyPhePheLeuThrAl 17

      78 GGTTATTGGAGATACTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAA 127
          :|||   ::::::   :::           |||:::        :::|||
      17 aValHisSerGluProAlaThrAlaCysGlyGluLysGlnTyrProVal. 33

     128 ATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAAT 177
           |||||||:::||||:|       |||       |||      |||   |||
      34 ..AsnSerLeuCysCysAspLeuCysProProGlyGlnLysLeuValAsn 49

     178 GACTGTCCAGCCCCGGGCAGGATACGGACTGCAGGGAGTGTGACAGCGG 227
          ||||||           ::::::   |||:::|||::::::|||   :::||
      50 AspCysThrGluValSerLys...ThrGluCysGlnSerCysGlyLysGl 65

     228 CTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTCAGCTGCTCCA 277
          |:::|||   ::::::   |||:::   :::::::|||   :::
      65 yGluPheLeuSerThrTrpAsnArgGluLysTyrCysHisGluHisArgT 82

     278 AATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTGCACAGTGGAC 327
            |||:::   ::::::|||                |||:::   |||::::::
      82 yrCysAsnProAsnLeuGlyLeuArgIleGlnSerGluGlyThrLeuAsn 98

     328 CGGCACACCCTGTGTGGCTCCAGGAAGAACCAGTACCGGCATTATTGGAG 377
            ||||||:::|||   |||    :::::::|||       |||      ||
      99 ThrAspThrIleCysValCysValGluGlyGln......HisCysThrSe 113

     378 TGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGG...A 424
          |::::::       :::|||          |||||||||||    |||
     113 rHisThrCysGluSerCysThrProHisSerLeuCysLeuProGlyPheG 130

     425 CCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGC...ACCTGC 471
```

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            |||            :::                :::||||||:|        |||
     130 lyValLysGlnIleAlaThrGlyLeuLeuAspThrValCysGluProCys 146

     472 CATGCAGGTTTCTTTCTAAGAGAAAACCAGTGTGTCTCCTGTAGTAACTG 521
                |||||||||            :::|||            :::    ::::::||
     147 ProLeuGlyPhePhe......SerAsnValSerSerAlaPheGluLysCy 161

     522 TAAGAAAAGGTGGAGTGCAGGAAGTTGTGCTACCCCAGATTGAGAATG 571
          |    :::          :::|||     :::        |||          :::|||:::
     161 sHisArgTrpThrSerCysGluArgLysGlyLeu......ValGluGlnH 176

     572 TTAAGGGCACT 582
             ||||||
     176 isValGlyThr 179
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